

What is claimed is:

1. A method for determining a proteasome inhibition therapy regimen for treating a tumor in a patient comprising:
 - a) determining the level of expression of at least one Predictive marker; and
 - b) determining a proteasome inhibition-based regimen for treating the tumor based on the expression of the predictive marker, wherein a significant expression level is indicative that the patient is either a responsive patient or a non-responsive patient.
2. The method of claim 1 wherein the level of expression of the predictive marker is determined by detection of mRNA.
3. The method of claim 1 wherein the level of expression of the predictive marker is determined by detection of protein.
4. The method of claim 1 wherein the predictive marker is selected from at least one of the markers identified in any of Table 1, Table 2, Table 3, Table 4 Table 5, Table 6, or Table 7.
5. The method of claim 1 wherein determining the significant level of expression is determined by comparison with a control marker or by comparison to a predetermined standard.
6. The method of claim 1, wherein the tumor is selected from liquid or solid tumors.
7. The method of claim 1 wherein the liquid tumor is selected from the group consisting of myelomas, multiple myeloma, Non-Hodgkins Lymphoma, B-cell lymphomas, Waldenstrom's syndrome, chronic lymphocytic leukemia, and other leukemias.
8. The method of claim 1 wherein the significant level expression is determined by a predictive marker set comprising two or more predictive markers.
9. The method of claim 1, wherein the proteasome inhibition-based regimen for treating the tumor comprises treatment with bortezomib.
10. The method of claim 1, wherein the patient sample comprising tumor cells is obtained from the subject any time selected from prior to tumor therapy, concurrently with tumor therapy or after tumor therapy.
11. A method for treating a tumor in a patient with a a proteasome inhibition therapy comprising:

a) determining the level of expression of at least one Predictive marker in a patient's tumor; and

b) treating the patient with proteasome inhibition therapy comprising a proteasome inhibitor agent based on the expression of the predictive marker, wherein a significant expression level is indicative that the patient is a responsive patient.

12. The method of claim 11 wherein the level of expression of the predictive marker is determined by detection of mRNA.

13. The method of claim 11 wherein the level of expression of the predictive marker is determined by detection of protein.

14. The method of claim 11 wherein the predictive marker is selected from at least one of the markers identified in any of Table 1, Table 2, Table 3, Table 4 Table 5, Table 6 or Table 7.

15. The method of claim 11 wherein determining the significant level of expression is determined by comparison with a control marker or by comparison to a predetermined standard.

16. The method of claim 11, wherein the tumor is selected from liquid or solid tumors.

17. The method of claim 11 wherein the liquid tumor is selected from the group consisting of multiple myeloma, Non-Hodgkins Lymphoma, B-cell lymphomas, mantle cell lymphoma, Waldenstrom's syndrome, chronic lymphocytic leukemia, and other leukemias.

18. The method of claim 11 wherein the significant level expression is determined by a predictive marker set comprising two or more predictive markers.

19. The method of claim 11, wherein the proteasome inhibition-based regimen for treating the tumor comprises treatment with a proteasome inhibitor is selected from the group consisting of a peptidyl aldehyde, a peptidyl boronic acid, a peptidyl boronic ester, a vinyl sulfone, an epoxyketone, and a lactacystin analog.

20. The method of claim 11, wherein the patient sample comprising tumor cells is obtained from the subject any time selected from prior to tumor therapy, concurrently with tumor therapy or after tumor therapy.

21. A marker set for use in the method of claim 1 comprising at least two isolated nucleic acid molecules selected from Table 1 Table 2 or Table 3.
22. A marker set for use in the method of claim 11 comprising at least two isolated nucleic acid molecules selected from Table 1 Table 2 or Table 3.
23. The marker set of claim 21 comprising a marker set constructed using the weighted voting method.
24. The marker set of claim 22 comprising a marker set constructed using the combination of threshold features model.
23. A kit for determining a proteasome inhibition therapy for treating a tumor in a patient comprising reagents for assessing the expression of at least one predictive marker, and instructions for use.
24. The kit of claim 23 wherein the reagents comprise one or a plurality of nucleic acid probes, wherein the probe specifically binds at least one predictive marker.
25. The kit of claim 23 wherein the reagents comprise at least one detecting reagent selected from the group consisting of an antibody, an antibody derivative, an antibody fragment, and peptide probe, wherein the antibody, antibody derivative, antibody fragment or peptide probe specifically binds to a protein corresponding to at least one predictive marker.
26. A method for identifying a candidate compound for treatment of cancer comprising
 - a) combining a composition comprising a polypeptide of one a predictive marker with a test compound;
 - b) determining whether the test compound binds the predictive marker polypeptide; and
 - c) identifying a compound which binds the predictive marker polypeptide as a candidate compound for treatment of cancer.